

SEQUENCE LISTING

<110> Sanjay Bhanot
Kenneth W. Dobie

<120> MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION

<130> RTS-0678US

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<210> 2

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<213> Artificial Sequence

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<223> Antisense Oligonucleotide

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<222> (231) ... (1397)

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ccgggacccc tgtgctctgc gcgaagccct ggccccgggg gccggggcat gggccagggg 180

cgcggggtga agcggttcc cgcgggggcg tgactgggcg ggcttcagcc atg aag 236

Met Lys

1

acc ctc ata gcc gcc tac tcc ggg gtc ctg cgc ggc gag cgt cag gcc 284

Thr Leu Ile Ala Ala Tyr Ser Gly Val Leu Arg Gly Glu Arg Gln Ala

5

10

15

gag gct gac cgg agc cag cgc tct cac gga gga cct gcg ctg tcg cgc 332

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Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser	Ile	Leu	Ser	Ala	Leu		
35					40					45					50		
cag gac ctc ttc tct gtc acc tgg ctc aat agg tcc aag gtg gaa aag 428																	
Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn	Arg	Ser	Lys	Val	Glu	Lys		
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cag cta cag gtc atc tca gtg ctc cag tgg gtc ctg tcc ttc ctt gta 476																	
Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln	Trp	Val	Leu	Ser	Phe	Leu	Val		
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ctg gga gtg gcc tgc agt gcc atc ctc atg tac ata ttc tgc act gat 524																	
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tgc tgg ctc atc gct gtg ctc tac ttc act tgg ctg gtg ttt gac tgg 572																	
Cys	Trp	Leu	Ile	Ala	Val	Leu	Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp		
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Thr	His	Asn	Leu	Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro		
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ctg gca ggc aac ttc cga atg cct gtg ttg agg gag tac ctg atg tct	860
Leu Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu Met Ser	
195 200 205 210	
gga ggt atc tgc cct gtc agc cgg gac acc ata gac tat ttg ctt tca	908
Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu Leu Ser	
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Lys Asn Gly Ser Gly Asn Ala Ile Ile Ile Val Val Gly Gly Ala Ala	
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gag tct ctg agc tcc atg cct ggc aag aat gca gtc acc ctg cgg aac	1004
Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr Leu Arg Asn	
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cgc aag ggc ttt gtg aaa ctg gcc ctg cgt cat gga gct gac ctg gtt	1052
Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly Ala Asp Leu Val	
260 265 270	
ccc atc tac tcc ttt gga gag aat gaa gtg tac aag cag gtg atc ttc	1100
Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr Lys Gln Val Ile Phe	
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att ggt ttc gcc cca tgc atc ttc cat ggt cga ggc ctc ttc tcc tcc	1196
Ile Gly Phe Ala Pro Cys Ile Phe His Gly Arg Gly Leu Phe Ser Ser	
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gac acc tgg ggg ctg gtg ccc tac tcc aag ccc atc acc act gtt gtg	1244
Asp Thr Trp Gly Leu Val Pro Tyr Ser Lys Pro Ile Thr Thr Val Val	
325 330 335	

gga gag ccc atc acc atc ccc aag ctg gag cac cca acc cag caa gac 1292
Gly Glu Pro Ile Thr Ile Pro Lys Leu Glu His Pro Thr Gln Gln Asp
340 345 350

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Ile Asp Leu Tyr His Thr Met Tyr Met Glu Ala Leu Val Lys Leu Phe
355 360 365 370

gac aag cac aag acc aag ttc ggc ctc ccg gag act gag gtc ctg gag 1388
Asp Lys His Lys Thr Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu
375 380 385

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Val Asn

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<213> Artificial Sequence

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<223> PCR Probe

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22

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<213> M. musculus

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<222> (207) ... (1373)

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agccctggcc ccggcggccg gggcatgggt caggggcgcg gcgtgaggcg gctttctgca 180

cggccgtgac gtgcattggc ttcagc atg aag acc ctc atc gcc gcc tac tcc 233

Met Lys Thr Leu Ile Ala Ala Tyr Ser

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5

ggg gtc ctg cgg ggt gag cgt cgg gcg gaa gct gcc cgc agc gaa aac 281

Gly Val Leu Arg Gly Glu Arg Arg Ala Glu Ala Ala Arg Ser Glu Asn

10

15

20

25

aag aat aaa gga tct gcc ctg tca cgc gag ggg tct ggg cga tgg ggc 329

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cta	caa	tgg	gtc	cta	tcc	ttc	ctg	gtg	cta	gga	gtg	gcc	tgc	agt	gtc	473	
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Ile	Leu	Met	Tyr	Thr	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu		
	90				95				100					105			
tac	ttc	acc	tgg	ctg	gca	ttt	gac	tgg	aac	acg	ccc	aag	aaa	ggc	ggc	569	
Tyr	Phe	Thr	Trp	Leu	Ala	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly	Gly		
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Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr	Phe	Arg		
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Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu	Leu	Thr	Thr		
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Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile	Met	Gly	Leu	Gly		
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gcc	ttc	tgt	aac	ttc	agc	aca	gag	gct	act	gaa	gtc	agc	aag	aag	ttt	761	
Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu	Val	Ser	Lys	Lys	Phe		
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cct ggc ata agg ccc tat ttg gct acg ttg gct ggt aac ttc cgg atg	809
Pro Gly Ile Arg Pro Tyr Leu Ala Thr Leu Ala Gly Asn Phe Arg Met	
190 195 200	
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Pro Val Leu Arg Glu Tyr Leu Met Ser Gly Gly Ile Cys Pro Val Asn	
205 210 215	
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Arg Asp Thr Ile Asp Tyr Leu Leu Ser Lys Asn Gly Ser Gly Asn Ala	
220 225 230	
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Ile Ile Ile Val Val Gly Gly Ala Ala Glu Ser Leu Ser Ser Met Pro	
235 240 245	
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Gly Lys Asn Ala Val Thr Leu Lys Asn Arg Lys Gly Phe Val Lys Leu	
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Ala Leu Arg His Gly Ala Asp Leu Val Pro Thr Tyr Ser Phe Gly Glu	
270 275 280	
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Asn Glu Val Tyr Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg	
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Trp Val Gln Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile	
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Phe His Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro	
315 320 325	
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Tyr Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Val Pro	
330 335 340 345	

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Lys Leu Glu His Pro Thr Gln Lys Asp Ile Asp Leu Tyr His Ala Met
350 355 360

tac atg gag gcc ctg gtg aag ctc ttt gac aat cac aag acc aaa ttt 1337
Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Asn His Lys Thr Lys Phe
365 370 375

ggc ctt cca gag act gag gtg ctg gag gtg aac tga cccagccctc 1383
Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn
380 385

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<400> 13

gggtgtggct caggaggat 19

<210> 14

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Probe

<400> 14

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18

<210> 15

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> PCR Primer

<400> 15

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<210> 16

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